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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Sat May 13 10:58:23 2000; MasPar time 3.90 Seconds 242.977 Million cell updates/sec

Title:

Description: Perfect Score: Sequence:

>US-09-331-631-8 (80-119) from US09331631.pep (3 of 4) 320 1 PEDPQRRYEECQQECRQQEERQQPQCQQRCLKRFEQEQQQ 40

Scoring table: РАМ 150 Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq35 1:geneseqp

Statistics: Mean 22.611; Variance 93.076; scale 0.243

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

23	22	21	20	19	18	17	16	15	14	13	12	11	10	ø	ω	7	σ	ഗ	4	w	N	1	No.
4 E	81	82	82	82	83	84	86	87	87	87	87	87	87	87	90	96	152	152	153	158	161	320	Score
	25.	25.	25.	25.	25	26.		27.	27.	27.	27.	27.2	27.	27.	28.	ω	47.		47.	49.4			Match
678	593	816	441	441	609	255	404	108	108	94	94	86	86	28	404	371	566	525	625	666	666	590	Length
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R42087	W62835	R71111	R89214	R41875	W83215	R74087	R27284	W95076	W95071	W95080	W95075	W95073	W95078	W62841	W14909	W73369	R20181	W62831	W62830	W62828	W62829	W62832	ID
D. melanogaster dorsal	Zea mays antimicrobial	Spinocerebellar ataxia	Peroxisome proliferato	Steroid hormone recept	Human h-NUMB-R.	Human receptor induced	Sequence encoded by th	sequence	Amino acid sequence of	GST-HD fusion protein			GST-HD fusion protein	Stenocarpus sinuatus a	yeast negat	Epitope tagged TBP pro	Sequence encoded by 67		Macadamia integrifolia	Macadamia integrifolia	mia i	Gossypium hirsutum ant	Description
8.62e+00	8.62e+00	7.	7.	7.12e+00	5.88e+00	4.85e+00		2.7	2.72e+00	2.72e+00	. 7	2.72e+00		2		4	•	.19e-	ω.	1.16e-	6.05e-	2.09e-23	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24
76	76	77	77	77	77	77	77	77	78	78	78	79	79	79	79	79	. 79	79	79	79	80
23.8	23.8	24.1	24.1	24.1	24.1	24.1	24.1	24.1	24.4	24.4	24.4	24.7	24.7	24.7	24.7	24.7	24.7	24.7	24.7	24.7	25.0
548	513	802	787	783	626	614	614	541	440	440	439	637	369	255	255	255	255	219	219	219	303
Н	<u>ب</u>	Н	щ	ш	<u>ب</u>	<u></u> _	سا	<b></b>	<u>ب</u>	<u></u>	Н	Н	Н	ш	_	_	Н	ட		<b></b> -	<b>ب</b>
W89189	W88413	W37153	W37152	W37151	W22150	W22149	W62834	W37148	R92479	W99597	R33745	W62837	W62647	W04174	R64197	W26658	R70977	W92523	W92524	W31759	R60054
Alternatively spliced,	Acute myeloid leukaemi	Mouse neural Mena+++ p	Mouse neural Mena++ pr	Mouse neural Mena+ pro	Peanut allergen Ara hI	Peanut allergen Ara hI	Arachis hypogaea antim	Mammalian Ena (Mena).	Peroxisome proliferato	Mouse peroxisome proli	XR4.	Hordeum vulgare antimi	Mature durum wheat glu	Human receptor H4-1BB.	Human 4-1BB polypeptid	Human 4-1BB receptor.	H4-1BB receptor protei	Human h4-1BBSV recepto	Human h4-1BBSV recepto	A novel human h4-1BBSV	Dirofilaria immitis pa
2.22e+01	2.22e+01	1.84e+01	1.84e+01	1.84e+01	1.84e+01	1.84e+01	1.84e+01	1.84e+01	1.52e+01	1.52e+01	1.52e+01	1.25e+01	1.26e+01	1.26e+01	1.26e+01	1.26e+01	1.26e+01	1.26e+01	1.26e+01	1.26e+01	1.04e+01

## ALIGNMENTS

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RESULT ID W AC W DT 2 DE M KW A FT P FT P FT P FT P FT P FT P FT O PD 0 PF 2 PR 2	Qu Be Ma Db	RESULTATION OF THE STATE OF THE
W62829; standard; Protein; 666 AA. W62829; 27-OCT-1998 (first entry) Macadamia integrifolia antimicrobial protein. Macadamia integrifolia. Macadamia integrifolia. Macadamia integrifolia. Mey Macadamia integrifolia. Mey Peptide Junctem "signal peptide" Protein Protein Protein Protein M09827805-A1. %notem "mature protein" %02-DEC-1998; AU-004275.	Query Match 100.0%; Score 320; DB 1; Length 590; Best Local Similarity 100.0%; Pred. No. 2.09e-22; Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 80 PEDPQRRYEECQQECRQQEERQQPQCQQRCLKRFEQEQQQ 119 80 PEDPQRRYEECQQECRQQEERQQPQCQQRCLKRFEQEQQQ 119	W62832 standard; Protein; 590 AA. W62832; 27-OCT-1998 (first entry) Gossypium hirsutum antimicrobial protein. antimicrobial protein; infestation; control. Gossypium hirsutum. C-JUL-1998. 27-DEC-1997; AU0874. 20-DEC-1996; AU-004275. (RETR-) COOP RES CENT TRODICAL PLANT PATHOLOGY. BOWER IN, Goulter KC, Green JL, Manners JM, Marcus JP; BOWER IN, Goulter KC, Green JE, Macadamia integrifolia - useful for controling microbial infestations of plants or mammals The sequence is that of an antimicrobial protein which can be used to control microbial infestations in plants and mammalian animals. Sequence 590 AA;

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N-PSDB; V42311.
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22-DEC-1997; AU0874.
20-DEC-1996; AU-004275.
(RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
BOWER NI, Goulter KC, Green JL, Manners JM, Mar
WPI; 98-377279/32.
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The sequence is that of an antimicrobial protein which can be used to control microbial infestations in plants and man
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The sequence is that of an antimicrobial protein which be used to control microbial infestations in plants animals.
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                                                                                                                                                                                                                                                                                   Macadamia integrifolia antimicrobial antimicrobial protein; infestation; c
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W62828;
27-OCT-1998 (first entry)
Macadamia integrifolia antimicrobial protein.
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9; Mismatches 9;
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Best Local S
Matches 1
                                                                                                                                                                                                                                                         26-DEC-1991.
07-JUN-1991; G00914.
11-JUN-1990; GB-013016.
(MRSC ) MARS UK LTD.
Spencer ME, Hodge R, Deakin EA
WPI; 92-024418/03.
expression vectors
Claim 4; Fig 2; 59pp;
The inventors claim a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-APR-1992 (first entry)
Sequence encoded by 67 kD T. c
Cocoa; flavour; vicilin; seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bower NI, Goulter KC, Green JL, Manners Bower NI, Goulter KC, Green JL, Manners WPI; 98-377279/32.

Novel anti-microbial protein from e.g. useful for controlling microbial infest Claim 1; Page 47-49; 96pp; English. The sequence is that of an antimicrobia
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The sequence is that of an antimicrobial protein which is the sequence of the sequence is that of an antimicrobial protein which is the sequence of the sequence is that of an antimicrobial infestations in plants because the sequence of the sequence is that of an antimicrobial infestations in plants
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22-DEC-1997; AU0874.
20-DEC-1996; AU-004275.
(RETR-) COOP RES CENT 1
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18; Conservative
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Green JL, Manners JM, Marcus
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Pred. No. 4.19e-06;
13; Mismatches 7;
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Pred. No. 3.38e-06;
10; Mismatches 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PT Transgenic animal expressing epitope-tagged TATA-box binding protein
PT for isolating higher-order transcription complexes and specific
PT factors that associate with the protein, useful as potential
PT therapeutic agents
PT therapeutic agents
PT Claim 5; Page 20-22; 38pp; English.
PT This sequence represents an epitope-tagged TATA-box binding protein (TBP)
CC This sequences by the transgenic non-human animals of the invention.
CC The animals are used to produce TBP. TBP is used to isolate and
CC characterise higher-order transcription complexes (from different tissue
CC and cell types, optionally at different developmental stages). It is also
CC used to identify new and/or specific TBP associated factors (TAFS,
CC e.g. transcription factors, activators or inhibitors) and TAF-interaction
CC factors, and to raise antibodies against TBP. The TAFS may be useful for
CC regulating gene expression, e.g. disease-related genes, so are potential
CC pharmaceuticals, also for identifying human analogues for use in drug
CC screening. The antibodies are used for affinity purification of TBP and
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 1
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Best Local S
Matches 1
               21-MAY-1997 (first entry)
Baker's yeast negative regulator of phospholipid biosynthesis.
Negative regulator of phospholipid biosynthesis; Opil protein;
leucine zipper; polyglutamine tract; inositol-1-phosphate.
Saccharomyces cerevisiae.
                                                                                                                                                                            LT 8
W14909 standard; Protein; 404
W14909;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W73369;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TBP associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                its complexes. TBP can isolate transcription complexes from a wide variety of different tissues and cells (contrast known methods that limited to isolation from a particular cell type). Sequence 371 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Berglund E, Kirschbaum B, Meisterernst M, Polites WPI; 99-001394/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
EP-881288-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATA-box binding
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26-MAY-1998; 109516.
26-MAY-1997; EP-108433.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                              storage proteins.
ence 566 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DPQRRYEECQQEC-RQQ-EERQQPQCQQRCLKRFEQEQQQ 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 47.5%;
Similarity 45.0%;
18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.0%;
larity 41.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TBP protein.
ng protein; epitope-tagged TBP; transcription complex; TAF; factor; TAF-interaction factor; gene expression regulator.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 96;
Pred. No.
13; Misma
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Pred. No. 4.19e-06;
13; Mismatches 7;
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Best Local 9
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04-FEB-1997.
14-JAN-1991;
14-JAN-1991;
02-DEC-1993;
30-MAY-1995;
                                                                                                                                                                                                                                                                                                                                              02-JUL-1998.
22-DEC-1997;
20-DEC-1996;
                                                                                                                                                                                        Novel anti-microbial protein from e.g. Macadamia integrifolia useful for controlling microbial infestations of plants or man Claim 1; Page 66; 96pp; Egglish.

The sequence is that of an antimicrobial protein which can
                                                                                                                                                                                                                                                                                                                                                                                                                                   Stenocarpus sinuatus antimicrobial protein. antimicrobial protein; infestation; control Stenocarpus sinuatus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the OPII gene encoding the present sequence have been deleted is claimed. The OPII gene encodes a negative regulator of phospholipid biosynthesis and the genetically engineered yeast cell is useful for enhanced production of inositol, inositol-containing metabolites or phospholipids, including myo-inositol and inositol-1-phosphate, for human or animal consumption.
                                                                                                                                                                                                                                                                                 (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY. Bower NI, Goulter KC, Green JL, Manners JM, Max WPI; 98-377279/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W62841;
27-OCT-1998 (first entry)
                                                                                                                          Sequence
                                                                                                                                                    apimals
                                                                                                                                                                        be used to control microbial infestations
                                                                                                                                                                                                                                                                                                                                                                                                                   WO9827805-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W62841 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Fig 8; 28pp; English.
A genetically engineered Saccharomyces yeast cell in which all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; T64394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Henry SA, White M WPI; 97-118296/11.
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DPIRQQQLCQMRCQQQEKDPRQQQQC
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US-640495.
US-165182.
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                                             Conservative
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/label=
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146
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153
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/note= "part of leucine zipper"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= DNA-binding_residue
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/note= "part of leucine zipper"
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"part of leucine zip
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Pred.
14; M
                                                           Score 87; I
Pred. No. 2.
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                                           Mismatches
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                                             DB 1,
2.72e+00;
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    lacking OPI1

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Misc\_difference

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a composition comprising a fusion protein of (i) (c) (poly)peptide that increases solubility and/or prevents aggregation of fusion protein, and (ii) amyloidogenic (poly)peptide that can self-cassemble into amyloid-like fibrils or protein aggregates. Host cells transformed with a vector containing the nucleic acid encoding the fusion protein are used for the recombinant expression of the fusion protein. The composition is used to detect onset and progression of diseases cassociated with fibrils/protein aggregates. It is potentially useful for treatment of such diseases (e.g. Alzheimer's disease, scrapie or CAG-crepeat expansion conditions such as Huntington's disease (HD), spinal and bulbar muscular atrophy, dentatorubral pallidolysian atrophy, spinal and concerebellar ataxia, Creutzfeld-Jakob disease). Assay methods based on release of the amyloidogenic polypeptide from fusion protein have a precise starting time for aggregate formation, allowing kinetic measurements, and use of an enzyme for cleavage allows testing under physiological conditions. Sequences W95077-80 represent GST-HD fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                        W95073 standard;
W95073;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteins.
Sequence
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31-JUL-1998; E04811.
31-JUL-1997; EP-113306.
01-AUG-1997; EP-113306.
(PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN Bates G, Lehrach H, Scherzinger E, Wanker E; WPI; 99-153775/13.
                                   Key
                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Composition containing fusion protein that includes amyloidogenic peptide - able to self-assemble into fibrils or aggregates, used detect and monitor neuronal diseases, and also to screen for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           therapeutic inhibitors
Disclosure; Fig 8; 62pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GST-HD fusion
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                                                                   sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
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                                                                                                                                                                                                                                                                                                                                                     Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86
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Pred.
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2.72e+00;
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cc aggregates, insoluble in detergents or urea. The method comprises: (a) cc applying material suspected of containing protein aggregates to a filter; cc and (b) detecting retention of protein aggregates on the filter. This cc method also helps to identify inhibitors of protein aggregates formation. Cc The method is particularly used to detect protein aggregates formation. Cc indicative of disease, for assessing onset or progression of the cc diseases. The inhibitors identified are potential therapeutic agents for treating the diseases. Other applications include detection of inclusion cc bodies in bacteria and to study kinetics of aggregate formation. Diseases associated with polyglutamine expansion are particularly diagnosed, e.g. Cc Huntington's, Alzheimer's or Parkinson's diseases; spinal and bulbar cc muscular atrophy; spinocerebellar ataxia; systemic amyloidosis; type II cc diabetes; bovine spongiform encephalopathy; kuru; familial insomnia; cc scrapie. The protein aggregates can now be detected simply, routinely and rapidly, without requiring sophisticated equipment. The method can be cc automated to allow many samples to be analysed on the same filter. Cc Sequences W95072-75 represent GST-HD fusion proteins.
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Best Local
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GST-HD fusion protein GST-HD51DELPBio.
GST-HD fusion protein GST-HD51DELPBio.
Amyloid-like fibril; protein aggregate; inhibitor; inclusion body;
polyglutamine expansion; Huntington's disease; Alzheimer's disease; HD;
polyglutamine expansion; Huntington's disease; Tophy; type II diabetes;
parkinson's disease; spinal; bulbar muscular atrophy; type II diabetes;
systemic amyloidosis; spinocerebellar ataxia; kuru; familial insomnia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W95075;
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31-JUL-1998; E04810.
01-AUG-1997; EP-113320.
(PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
Bates G, Lehrach H, Scherzinger E, Wanker E;
WPI; 99-15395/13.
Detecting amyloid-like fibrils or protein aggregates insoluble in detergent or urea - from their retention on a filter, used for diagnosis, particularly of diseases associated with polyglutamine
                                          Detecting amyloid-like fibrils or protein aggregates insoluble in detergent or urea - from their retention on a filter, used for diagnosis, particularly of diseases associated with polyglutamine
                                                                                                                     11-FEB-1999.
31-JUL-1998; E04810.
01-AUG-1997; EP-113320.
(PLAC ) MAX PLANCK GES FOERDERUNG Bates G, Lehrach H, Scherzinger E, WPI; 99-153955/13.
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The invention relates to the detection of amyloid-like fibrils or protein aggregates, insoluble in detergents or urea. The method comprises: (a)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expansion
  Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     bovine spongiform encephalopathy; kuru;
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                                                                                                                                                                                                                                                                                                                                                                                          sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 27.2%;
Similarity 34.2%;
13; Conservative
  Fig 8; 56pp;
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                                                                                                                                                                                                                                                                                           /note= "this residue which is not
                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
English
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15; N
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Pred. No. 2.72e+00
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                                                                                                                                                 WISSENSCHAFTEN
, Wanker E;
                                                                                                                                                                                                                                                                                           is connected indicated in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is connected indicated in
                                                                                                                                                                                                                                                                                                                                                                                                                                          scrapie; GST-HD;
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the sequence"
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                                                                                                                                                                                                                                                                                             sequence"
                                                                                                                                                                                                                                                                                                                      GST protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                          fusion protein
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Query Match
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Thes 13; Conser
ps Disclosure; Fig 8; 62pp; English.

CC The invention relates to a composition comprising a fusion protein of (i) (c) (poly)peptide that increases solubility and/or prevents aggregation of (i) (foly)peptide that increases solubility and/or prevents aggregation of (ii) (solub) protein, and (ii) amyloidogenic (poly)peptide that can self-composition protein, amyloidogenic (poly)peptide that can self-composition amyloidogenic (poly)peptide that can self-composition is used for the recombinant expression of the fusion protein.

CC The composition is used to detect onset and progression of diseases cassociated with fibrils/protein aggregates. It is potentially useful for treatment of such diseases (e.g. Alzheimer's disease, scrapie or CAG-crepeat expansion conditions such as Huntington's disease (HD), spinal and bulbar muscular atrophy, dentatorubral pallidoluysian atrophy, spinal and spinocerebellar ataxia, Creutzfeld-Jakob disease). Assay methods based on crelease of the amyloidogenic polypeptide from fusion protein have a precise starting time for aggregate formation, allowing kinetic measurements, and use of an enzyme for cleavage allows testing under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-MAY-1999 (first entry)

6ST-HD fusion protein GST-HD51DELPBio.

Fusion protein; amyloidogenic polypeptide; amyloid-like fibril; scrapie; protein aggregate; Alzheimer's disease; CAG-repeat expansion; spinal; Huntington's disease; bulbar muscular atrophy; spinocerebellar ataxia; dentatorubral pallidoluysian atrophy; Creutzfeld-Jakob disease; enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         associated with polyglutamine expansion are particularly diagnosed, e.g. Huntington's, Alzheimer's or Parkinson's diseases; spinal and bulbar muscular atrophy; spinocerebellar ataxia; systemic amyloidosis; type II diabetes; bovine spongiform encephalopathy; kuru; familial insomnia; scrapie. The protein aggregates can now be detected simply, routinely and rapidly, without requiring sophisticated equipment. The method can be made quantitative, by analysing a series of dilutions, and can be automated to allow many samples to be analysed on the same filter. Sequences W95072-75 represent GST-HD fusion proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Composition containing fusion protein that includes amyloidogenic peptide - able to self-assemble into fibrils or aggregates, used detect and monitor neuronal diseases, and also to screen for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-FEB-1999.
31-JUL-1998; E04811.
01-AUG-1997; EP-113306.
(PLAC ) MAX PLANCK GES FOERDERUNG Rates G, Lehrach H, Scherzinger E, WPI; 99-153775/13.
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W95080 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                           therapeutic inhibitors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to aggregates, insoluble in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DPQRRYEECQQECRQQEERQQPQCQQRCLKRFEQEQQQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.2%;
llarity 34.2%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "this residue which is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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detergents or urea. The method comprises:
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15; M
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82 19

DPQRRYEECQQECRQQEERQQPQCQQRCLKRFEQEQQQ 

119

Query Match

Similarity 34.28 13; Conservative

27.2%;

Score 87; Pred. No. Pred. 15; 1

2.72e+00 DB 1;

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                   method also helps to identify inhibitors of protein aggregates formation. CC The method is particularly used to detect protein aggregates that are indicative of disease, for assessing onset or progression of the CC diseases. The inhibitors identified are potential therapeutic agents for treating the diseases. Other applications include detection of inclusion co bodies in bacteria and to study kinetics of aggregate formation. Diseases associated with polyglutamine expansion are particularly diagnosed, e.g. Huntington's, Alzheimer's or Parkinson's diseases; spinal and bulbar muscular atrophy; spinocerebellar ataxia; systemic amyloidosis; type II cabbetes; bovine spongiform encephalopathy; kuru; familial insomnia; crapidly, without requiring sophisticated equipment. The method can be automated to allow many samples to be analysed on the same filter. The product which is connected to a GST protein to form a fusion protein. The aggregates of the GST protein is not indicated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local 9
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01-AUG-1997; EP-113320.
(PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
Bates G, Lehrach H, Scherzinger E, Wanker E;
WPI; 99-153955/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-MAY-1999 (first entry)
Amino acid sequence of Huntington's gene exon 1 in GST-HD fusion prote
Amyloid-like fibril; protein aggregate; inhibitor; inclusion body;
polyglutamine expansion; Huntington's disease; Alzheimer's disease;
Parkinson's disease; spinal; bulbar muscular atrophy; type II diabetes
systemic amyloidosis; spinocerebellar ataxia; kuru; familial insomnia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W95071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              physiological conditions. proteins. Sequence 94 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aggregates, insoluble in detergents or urea. The method comprises: (a) applying material suspected of containing protein aggregates to a filter; and (b) detecting retention of protein aggregates on the filter. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to the detection of aggregates, insoluble in detergents or un
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detecting amyloid-like fibrils or protein aggregates insoluble detergent or urea - from their retention on a filter, used for diagnosis, particularly of diseases associated with polyglutamic
   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Fig 2; 56pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-FEB-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bovine spongiform encephalopathy; kuru;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-MAY-1999
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13; Conser
      108
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ilarity 34.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "GST protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "polyglutamine expansion that can comprise
    upto 51 glutamines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 87;
Pred. No.
15; Mismai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A
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2.72e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amyloid-like
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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Search completed: Sat May 13 10:58:32 2000 Job time : 9 secs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a composition comprising a fusion protein of (i) (C (poly)peptide that increases solubility and/or prevents aggregation of tusion protein, and (ii) amyloidogenic (poly)peptide that can self-cc assemble into amyloid-like fibrils or protein aggregates. Host cells transformed with a vector containing the nucleic acid encoding the fusion protein are used for the recombinant expression of the fusion protein. CC The composition is used to detect onset and progression of diseases cc associated with fibrils/protein aggregates. It is potentially useful for treatment of such diseases (e.g. Alzhelmer's disease, scrapie or CAG-crepeat expansion conditions such as Huntington's disease (HD), spinal and CC bulbar muscular atrophy, dentatorubral pallidolysian atrophy, spinal and CC spinocerebellar ataxia, Creutzfeld-Jakob disease). Assay methods based on crelease of the amyloidogenic polypeptide from fusion protein have a precise starting time for aggregate formation, allowing kinetic measurements, and use of an enzyme for cleavage allows testing under CC physiological conditions. The present sequence represents the funtington's gene exon 1 translation product which is connected to a CST protein to form a fusion protein. The sequence of the GST protein is not indicated.
                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 1
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W95076;
W95076;
20-MAY-1999 (first entry)
Amino acid sequence of Huntington's gene exon 1 in GST-HD fusion protein.
Fusion protein; amyloidogenic polypeptide; amyloid-like fibril; scrapie;
protein aggregate; Alzheimer's disease; CAG-repeat expansion; spinal;
Huntington's disease; bulbar muscular atrophy; spinocerebellar ataxia;
dentatorubral pallidoluysian atrophy; Creutzfeld-Jakob disease; enzyme;
GST-HD; HD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Composition containing fusion protein that includes amyloidogenic peptide - able to self-assemble into fibrils or aggregates, used to detect and monitor neuronal diseases, and also to screen for therapeutic inhibitors

Example 1; Fig 2; 62pp; English.
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31-JUL-1998; E04811.
01-AUG-1997; EP-113306.
(PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
Bates G, Lehrach H, Scherzinger E, Wanker E;
WPI; 99-153775/13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                            y Match 27.2%;
Local Similarity 34.2%;
nes 13; Conservative
                                                                                                                                                      82 DPQRRYEECQQECRQQEERQQPQCQQRCLKRFEQEQQQ 119
                                                                                                                                                                                                                         19 ΕSIKSFQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 AA;
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    upto 51 glutamines"
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Pred. No. 2.72e+00;
15; Mismatches 10
                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                                                                                   Length 108;
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